

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/500,377
Source: JFW16
Date Processed by STIC: 03/02/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/02/2006

PATENT APPLICATION: US/10/500,377

TIME: 14:01:52

Input Set : A:\Final Sequence list-12810-00139-US.txt

Output Set: N:\CRF4\03022006\J500377.raw

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3 <110> APPLICANT: Nasholm, Torgny
4     Erikson, Oskar
5     Hertzberg, Magnus
7 <120> TITLE OF INVENTION: Selective plant growth using D-amino acids
9 <130> FILE REFERENCE: 12810-00139-US
11 <140> CURRENT APPLICATION NUMBER: US 10/500,377
12 <141> CURRENT FILING DATE: 2004-06-30
14 <150> PRIOR APPLICATION NUMBER: PCT/EP03/00222
15 <151> PRIOR FILING DATE: 2003-01-13
17 <150> PRIOR APPLICATION NUMBER: GB 0201043.7
18 <151> PRIOR FILING DATE: 2002-01-17
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 38
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of artificial sequence: primer
32 <400> SEQUENCE: 1
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36 <210> SEQ ID NO: 2
37 <211> LENGTH: 35
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Description of artificial sequence: primer
44 <400> SEQUENCE: 2
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48 <210> SEQ ID NO: 3
49 <211> LENGTH: 30
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Description of artificial sequence: primer
56 <400> SEQUENCE: 3
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60 <210> SEQ ID NO: 4
61 <211> LENGTH: 30
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of artificial sequence: primer

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68 <400> SEQUENCE: 4
69 attagatcta cagccacaat tcccccccta 30
72 <210> SEQ ID NO: 5
73 <211> LENGTH: 1160
74 <212> TYPE: DNA
75 <213> ORGANISM: Rhodosporidium toruloides
77 <400> SEQUENCE: 5
78 atgcactcgc agaagcgcgt cggtgtcctc ggatcaggcg ttatcggctc gagcagcgcc 60
80 ctcatcctcg ctcggaaggg ctacagcggtg catattctcg cgcgcgactt gccggaggac 120
82 gtctcgagcc agactttcgc ttcacccatgg gctggcgcgga attggacgcc ttctcatgacg 180
84 cttacagacg gtcctcgaca agcaaaatgg gaagaatcga ctttcaagaa gtgggtcgag 240
86 ttgggtccga cgggccatgc catgtggctc aaggggacga ggcgggttcgc gcagaacgaa 300
88 gacggcttgc tcgggcactg gtacaaggac atcacgccaa attaccgccc cctcccctct 360
90 tccgaatgtc cacctggcgc tatcggcgta acctacgaca ccctctccgt ccacgcacca 420
92 aagtactgcc agtaccttgc aagagagctg cagaagctcg gcgcgacgtt tgagagacgg 480
94 accgttacgt cgcttgagca ggcgttcgac ggtgcggatt tgggtggtaa cgctacggga 540
96 cttggcgcca agtcgattgc gggcatcgac gaccaagccg ccgagccaat ccgcgggcaa 600
98 accgtcctcg tcaagtcccc atgcaagcga tgcacgatgg actcgtccga ccccgcttct 660
100 cccgcctaca tcattccccg accaggtggc gaagtcactc gggcggggac gtacggcggtg 720
102 ggagactggg acttgtctgt caaccagag acggtccagc ggatcctcaa gcaactgcttg 780
104 cgcctcgacc cgaccatctc gagcgacgga acgatcgaag gcacgcaggt cctccgccac 840
106 aacgtcggct tgcgacctgc acgacgagggc ggaccccgcg ttgaggcaga acggatcgctc 900
108 ctgcctctcg accggacaaa gtcgcccctc tcgctcgga ggggcagcgc acgagcggcg 960
110 aaggagaagg aggtcacgct tgtgcatgct tatggcttct cgagtgcggg ataccagcag 1020
112 agttggggcg cggcgaggga tgtcgcgacg ctgctcgacg aggcgttcca gcggtaccac 1080
114 ggcgcggcgc gggagtcgaa gttgtagggc gggatttgtg gctgtattgc gggcatctac 1140
116 aagaaaaaaaa aaaaaaaaaa
119 <210> SEQ ID NO: 6
120 <211> LENGTH: 368
121 <212> TYPE: PRT
122 <213> ORGANISM: Rhodosporidium toruloides
124 <400> SEQUENCE: 6
126 Met His Ser Gln Lys Arg Val Val Val Leu Gly Ser Gly Val Ile Gly
127 1 5 10 15
130 Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile
131 20 25 30
134 Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser
135 35 40 45
138 Pro Trp Ala Gly Ala Asn Trp Thr Pro Phe Met Thr Leu Thr Asp Gly
139 50 55 60
142 Pro Arg Gln Ala Lys Trp Glu Glu Ser Thr Phe Lys Lys Trp Val Glu
143 65 70 75 80
146 Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe
147 85 90 95
150 Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr
151 100 105 110
154 Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile
155 115 120 125
158 Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln

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159      130      135      140
162 Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg
163 145      150      155      160
166 Thr Val Thr Ser Leu Gln Ala Phe Asp Gly Ala Asp Leu Val Val
167      165      170      175
170 Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln
171      180      185      190
174 Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys
175      195      200      205
178 Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile
179      210      215      220
182 Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val
183 225      230      235      240
186 Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu
187      245      250      255
190 Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile
191      260      265      270
194 Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg
195      275      280      285
198 Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp
199      290      295      300
202 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala
203 305      310      315      320
206 Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala
207      325      330      335
210 Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val
211      340      345      350
214 Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
215      355      360      365
218 <210> SEQ ID NO: 7
219 <211> LENGTH: 1989
220 <212> TYPE: DNA
221 <213> ORGANISM: Escherichia coli
223 <400> SEQUENCE: 7
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226 ccagcatatg agcatgggga cgatgctcac acatacggaa aatggcttcg gttctattgc 120
228 taatattttg ctgattatcg gggccggagg cgcattcaac gcattttaaa aagcagcagt 180
230 ctcgctgata cgctggcagt tattctctcc aatatgcata tgcacccgat tcttctggcc 240
232 tggtagtgag ctcttattct gcatgcggca gtgggctccg ctaccgtggc aatgatgggg 300
234 gcaacggcaa ttgttgacc catgctgccg ctgtatcccg acatcagccc ggaaattatt 360
236 gcgattgcta tcggttcagg tgcaattggc tgcactatcg ttacggactc gcttttctgg 420
238 ctagtgaagc aatattgcgg cgctacgctc aatgaaacat ttaaatacta tacgacagcg 480
240 acatttatcg cttcagtcgt cgctctggcg ggcacattcc tgctgtcatt tatcatctaa 540
242 gcgcaaagag acgtactatg gaaaacgcta aaatgaactc gctcatcgcc cagtatccgt 600
244 tggtaaagga tctggttgct cttaaagaaa ccacctggtt taatcctggc acgacctcat 660
246 tggctgaagg tttaccttat gttggcctga ccgaacagga tgttcaggac gcccatgcgc 720
248 gcttatcccg ttttgacccc tatctggcaa aagcatttcc tgaaactgct gccactgggg 780
250 ggattattga atcagaactg gttgccattc gagctatgca aaaacggctg gaaaaagaat 840
252 atcagcaacc gatcagcggg caactgttac tgaaaaaaga tagccatttg cccatttccg 900

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254 gctccataaa agcacgcggc gggatttatg aagtcctggc acacgcagaa aaactggctc 960
256 tggaagcggg gttgctgacg cttgatgatg actacagcaa actgctttct ccggagttta 1020
258 aacagttctt tagccaatac agcattgctg tgggctcaac cggaaatctg gggttatcaa 1080
260 tcggcattat gagcgcccgc attggcttta aggtgacagt tcatatgtct gctgatgcc 1140
262 gggcatggaa aaaagcgaaa ctgcgcacgc atggcggttac ggtcgtggaa tatgagcaag 1200
264 attatggtgt tgccgtcgag gaaggacgta aagcagcgca gtctgaccgc aactgtttct 1260
266 ttattgatga cgaaaattcc cgcacgttgt tccttgggta ttccgtcgct ggccagcgct 1320
268 ttaaagcgca atttgccag caaggccgta tcgtcgatgc tgataaccct ctgtttgtct 1380
270 atctgccgtg tgggtgttggc ggtggtcctg gtggcgctgc attcgggctt aaactggcgt 1440
272 ttggcgatca tgttactgc ttttttgcg aaccaacgca ctccccttgt atgttgtag 1500
274 gcgtccatac aggattacac gatcagattt ctgttcagga tattggtatc gacaacctta 1560
276 ccgcagcggg tggccttgca gttggtcgcg catcaggctt tgcggggcgg gcaatggagc 1620
278 gtctgctgga tggcttctat acccttagcg atcaaaccat gtatgacatg cttggctggc 1680
280 tggcgcagga agaaggtatt cgtctgaac cttcggcact ggcgggtatg gccggacctc 1740
282 agcgcgtgtg tgcacagta agttaccaac agatgcacgg ttccagcgca gaacaactgc 1800
284 gtaataccac tcatctggtg tgggcgacgg gaggtggaat ggtgccggaa gaagagatga 1860
286 atcaatatct ggcaaaaggc cgtaataaac gtttcaacgc agcatcgcaa tcctttccct 1920
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290 cctcctttt

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295 <210> SEQ ID NO: 8

296 <211> LENGTH: 442

297 <212> TYPE: PRT

298 <213> ORGANISM: Escherichia coli

300 <400> SEQUENCE: 8

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306 Lys Asp Leu Val Ala Leu Lys Glu Thr Thr Trp Phe Asn Pro Gly Thr
307 20 25 30
310 Thr Ser Leu Ala Glu Gly Leu Pro Tyr Val Gly Leu Thr Glu Gln Asp
311 35 40 45
314 Val Gln Asp Ala His Ala Arg Leu Ser Arg Phe Ala Pro Tyr Leu Ala
315 50 55 60
318 Lys Ala Phe Pro Glu Thr Ala Ala Thr Gly Gly Ile Ile Glu Ser Glu
319 65 70 75 80
322 Leu Val Ala Ile Pro Ala Met Gln Lys Arg Leu Glu Lys Glu Tyr Gln
323 85 90 95
326 Gln Pro Ile Ser Gly Gln Leu Leu Leu Lys Lys Asp Ser His Leu Pro
327 100 105 110
330 Ile Ser Gly Ser Ile Lys Ala Arg Gly Gly Ile Tyr Glu Val Leu Ala
331 115 120 125
334 His Ala Glu Lys Leu Ala Leu Glu Ala Gly Leu Leu Thr Leu Asp Asp
335 130 135 140
338 Asp Tyr Ser Lys Leu Leu Ser Pro Glu Phe Lys Gln Phe Phe Ser Gln
339 145 150 155 160
342 Tyr Ser Ile Ala Val Gly Ser Thr Gly Asn Leu Gly Leu Ser Ile Gly
343 165 170 175
346 Ile Met Ser Ala Arg Ile Gly Phe Lys Val Thr Val His Met Ser Ala
347 180 185 190
350 Asp Ala Arg Ala Trp Lys Lys Ala Lys Leu Arg Ser His Gly Val Thr

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351          195          200          205
354 Val Val Glu Tyr Glu Gln Asp Tyr Gly Val Ala Val Glu Glu Gly Arg
355          210          215          220
358 Lys Ala Ala Gln Ser Asp Pro Asn Cys Phe Phe Ile Asp Asp Glu Asn
359 225          230          235          240
362 Ser Arg Thr Leu Phe Leu Gly Tyr Ser Val Ala Gly Gln Arg Leu Lys
363          245          250          255
366 Ala Gln Phe Ala Gln Gln Gly Arg Ile Val Asp Ala Asp Asn Pro Leu
367          260          265          270
370 Phe Val Tyr Leu Pro Cys Gly Val Gly Gly Gly Pro Gly Gly Val Ala
371          275          280          285
374 Phe Gly Leu Lys Leu Ala Phe Gly Asp His Val His Cys Phe Phe Ala
375          290          295          300
378 Glu Pro Thr His Ser Pro Cys Met Leu Leu Gly Val His Thr Gly Leu
379 305          310          315          320
382 His Asp Gln Ile Ser Val Gln Asp Ile Gly Ile Asp Asn Leu Thr Ala
383          325          330          335
386 Ala Asp Gly Leu Ala Val Gly Arg Ala Ser Gly Phe Val Gly Arg Ala
387          340          345          350
390 Met Glu Arg Leu Leu Asp Gly Phe Tyr Thr Leu Ser Asp Gln Thr Met
391          355          360          365
394 Tyr Asp Met Leu Gly Trp Leu Ala Gln Glu Glu Gly Ile Arg Leu Glu
395          370          375          380
398 Pro Ser Ala Leu Ala Gly Met Ala Gly Pro Gln Arg Val Cys Ala Ser
399 385          390          395          400
402 Val Ser Tyr Gln Gln Met His Gly Phe Ser Ala Glu Gln Leu Arg Asn
403          405          410          415
406 Thr Thr His Leu Val Trp Ala Thr Gly Gly Gly Met Val Pro Glu Glu
407          420          425          430
410 Glu Met Asn Gln Tyr Leu Ala Lys Gly Arg
411          435          440

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VERIFICATION SUMMARY

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